



Sequences producing significant alignments:

Score E
(bits) Value

| | | | | |
|---|--------------------------------------|------------|-------|--|
| <u>gi 9755159 gb AAF98175.1 AF285167_1</u> | ATP-binding cassette tr... | <u>589</u> | e-167 | |
| <u>gi 13876613 gb AAK43526.1 AF287262_1</u> | ATP-binding cassette 1... | <u>589</u> | e-167 | |
| <u>gi 21536376 ref NP_005493.2 </u> | ATP-binding cassette, sub-fami... | <u>588</u> | e-167 | |
| <u>gi 9247086 gb AAF86276.1 AF275948_1</u> | ABCA1 [Homo sapiens] | <u>585</u> | e-166 | |
| <u>gi 5734135 gb AAD49852.1 </u> | ATP cassette binding transporter ... | <u>585</u> | e-166 | |
| <u>gi 4128033 emb CAA10005.1 </u> | ATP-binding cassette transporter... | <u>585</u> | e-166 | |
| <u>gi 13123945 sp O95477 ABC1_HUMAN</u> | ATP-binding cassette, sub-... | <u>585</u> | e-166 | |
| <u>gi 7304849 ref NP_038482.1 </u> | ATP-binding cassette 1, sub-fam... | <u>549</u> | e-155 | |
| <u>gi 13124694 sp P41233 ABC1_MOUSE</u> | ATP-binding cassette, sub-... | <u>549</u> | e-155 | |
| <u>gi 11611825 gb AAG39073.1 AF287263_1</u> | ATP-binding cassette 1... | <u>541</u> | e-153 | |
| <u>gi 27714435 ref XP_232954.1 </u> | similar to ABCA1 [Homo sapiens...] | <u>498</u> | e-140 | |
| <u>gi 18028983 gb AAL56247.1 AF362377_1</u> | ATP-binding cassette t... | <u>472</u> | e-132 | |
| <u>gi 27806343 ref NP_776646.1 </u> | ATP-binding cassette, sub-fami... | <u>288</u> | 4e-77 | |
| <u>gi 2959643 gb AAC05632.1 </u> | rim ABC transporter [Homo sapiens] | <u>287</u> | 9e-77 | |
| <u>gi 2969966 emb CAA75729.1 </u> | ABCR [Homo sapiens] | <u>287</u> | 1e-76 | |
| <u>gi 6707663 sp P78363 ABCR_HUMAN</u> | Retinal-specific ATP-bindin... | <u>287</u> | 1e-76 | |
| <u>gi 4557876 ref NP_000341.1 </u> | ATP-binding cassette, sub-famil... | <u>287</u> | 1e-76 | |
| <u>gi 3243082 gb AAC23915.1 </u> | ATP-binding cassette transporter ... | <u>287</u> | 1e-76 | |
| <u>gi 6671495 ref NP_031404.1 </u> | ATP-binding cassette, sub-famil... | <u>286</u> | 3e-76 | |
| <u>gi 12656651 gb AAK00959.1 AF328787_1</u> | ABC transporter member... | <u>244</u> | 1e-63 | |
| <u>gi 15451838 ref NP_150651.1 </u> | ATP-binding cassette, sub-fami... | <u>243</u> | 3e-63 | |

| | | | |
|--------------------------------------|---|-----|-------|
| gi 9506365 ref NP_061985.1 | ATP-binding cassette, sub-famil... | 242 | 5e-63 |
| gi 22725156 gb AAN04657.1 | ABC transporter ABCA7 [Homo sapi... | 241 | 8e-63 |
| gi 15451840 ref NP_038878.1 | ATP-binding cassette, sub-fami... | 239 | 3e-62 |
| gi 26342298 dbj BAC34811.1 | unnamed protein product [Mus mu... | 228 | 7e-59 |
| gi 20521748 dbj BAA83014.2 | KIAA1062 protein [Homo sapiens] | 100 | 4e-20 |
| gi 11346269 pir A59189 | ATP-binding cassette transporter - ... | 98 | 1e-19 |
| gi 14916523 sp Q9BZC7 ABC2_HUMAN | ATP-binding cassette, sub-... | 98 | 1e-19 |
| gi 14550412 ref NP_001597.1 | ATP-binding cassette, sub-fami... | 98 | 1e-19 |
| gi 11993939 ref NP_031405.1 | ATP-binding cassette, sub-fami... | 97 | 2e-19 |
| gi 14250599 gb AAH08755.1 AAH08755 | Similar to KIAA1062 prot... | 97 | 3e-19 |
| gi 1082239 pir B54774 | ATP binding cassette transporter ABC... | 96 | 7e-19 |
| gi 13242308 ref NP_077372.1 | ATP-binding cassette, sub-fami... | 95 | 1e-18 |
| gi 27881503 ref NP_775099.1 | ATP-binding cassette, sub-fami... | 82 | 1e-14 |
| gi 27881501 ref NP_056472.2 | ATP-binding cassette, sub-fami... | 82 | 1e-14 |
| gi 23957299 gb AAN40735.1 AF418105_1 | ATP-binding cassette t... | 82 | 1e-14 |
| gi 14189735 gb AAK54355.1 | ATP-binding cassette transporter... | 82 | 1e-14 |
| gi 27684549 ref XP_237242.1 | similar to ATP-binding casset... | 75 | 1e-12 |
| gi 25141343 ref NP_490949.2 | ABC transporter family member ... | 72 | 1e-11 |
| gi 7498949 pir T15200 | hypothetical protein F12B6.1 - Caeno... | 71 | 2e-11 |
| gi 21297828 gb EAA09973.1 | agCP11808 [Anopheles gambiae str... | 59 | 1e-07 |
| gi 20850354 ref XP_136692.1 | similar to ATP-binding casset... | 58 | 1e-07 |
| gi 24643648 ref NP_608437.1 | CG1819-PA [Drosophila melanoga... | 47 | 3e-04 |
| gi 27697650 ref XP_223630.1 | similar to hypothetical protei... | 39 | 0.11 |
| gi 15610478 ref NP_217859.1 | hypothetical protein Rv3342 [M... | 34 | 2.3 |
| gi 15842938 ref NP_337975.1 | methyltransferase, putative [M... | 34 | 2.4 |
| gi 20088939 ref NP_615014.1 | conserved hypothetical protein... | 34 | 2.6 |
| gi 1172578 sp Q08304 PPOB_LYCES | Polyphenol oxidase B, chlor... | 34 | 2.8 |
| gi 20899064 ref XP_139895.1 | similar to ATP-binding casset... | 33 | 3.2 |
| gi 21227448 ref NP_633370.1 | Fe-S oxidoreductase [Methanosa... | 33 | 4.3 |
| gi 27378790 ref NP_770319.1 | blr3679 [Bradyrhizobium japoni... | 33 | 5.1 |

Alignments

Get selected sequences Select all Deselect all

>gi|9755159|gb|AAF98175.1|AF285167_1 ATP-binding cassette transporter 1 [Homo Length = 2261

Score = 589 bits (1519), Expect = e-167
 Identities = 283/284 (99%), Positives = 283/284 (99%)

Query: 1 FGKYPSELQWPWMYNENYTFVSNDAPEDGTLELLNALTDPFGTRCMEGNPIPDTPCQ 60
 FGKYPSELQWPWMYNE YTFVSNDAPEDGTLELLNALTDPFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELQWPWMYNEQYTFVSNDAPEDGTLELLNALTDPFGTRCMEGNPIPDTPCQ 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVNSNTQALPPSQE 180

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 1550

Query: 181 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 240
 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN
 Sbjct: 1551 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1611 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

[>] >gi|13876613|gb|AAK43526.1|AF287262_1 ATP-binding cassette 1 sub-family A member
 Length = 2261

Score = 589 bits (1519), Expect = e-167
 Identities = 283/284 (99%), Positives = 283/284 (99%)

Query: 1 FGKYPSELQPWMYNE NYTFVSNDAPEDGTLELLNAL TD PGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELQPWMYNE YTFVSNDAPEDGTLELLNAL TD PGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELQPWMYNE QYTFVSNDAPEDGTLELLNAL TD PGFGTRCMEGNPIPDTPCQ 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPQRK
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 180
 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 1550

Query: 181 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 240
 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN
 Sbjct: 1551 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1611 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

[>] >gi|21536376|ref|NP_005493.2| [>] ATP-binding cassette, sub-family A member 1; ATI
 high density lipoprotein deficiency, Tangier type, 1;
 cholesterol efflux regulatory protein [Homo sapiens]
 gi|15212107|dbj|BAB63210.1| ABCA1 [Homo sapiens]
 Length = 2261

Score = 588 bits (1515), Expect = e-167
 Identities = 282/284 (99%), Positives = 283/284 (99%)

Query: 1 FGKYPSELQPWMYNE NYTFVSNDAPEDGTLELLNAL TD PGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELQPWMYNE YTFVSNDAPEDGTLELLNAL TD PGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELQPWMYNE QYTFVSNDAPEDGTLELLNAL TD PGFGTRCMEGNPIPDTPCQ 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPQRK
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 180

QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 1550

Query: 181 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 240
 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDT+NNVKWFNNKGWHAISSFLNVIN
 Sbjct: 1551 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTKNNVKWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1611 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

[>] >gi|9247086|gb|AAF86276.1|AF275948_1 [Homo sapiens]
 Length = 2261

Score = 585 bits (1509), Expect = e-166
 Identities = 281/284 (98%), Positives = 281/284 (98%)

Query: 1 FGKYPSELQPWMYNEYTFVSNDAPEDTGTELLNALTDPFGTRCMEGNPIPDTPCQ 60
 FGKYPSELQPWMYNE YTFVSNDAPEDTGTELLNALTDPFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELQPWMYNEQYTFVSNDAPEDTGTELLNALTDPFGTRCMEGNPIPDTPCQ 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWMTQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWMTQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWMTQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 180
 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 1550

Query: 181 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 240
 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN
 Sbjct: 1551 VNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTTSVD
 Sbjct: 1611 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVA XMTTSVD 1654

[>] >gi|5734135|gb|AAD49852.1| ATP cassette binding transporter 1 [Homo sapiens]
 Length = 849

Score = 585 bits (1507), Expect = e-166
 Identities = 282/284 (99%), Positives = 283/284 (99%)

Query: 1 FGKYPSELQPWMYNEYTFVSNDAPEDTGTELLNALTDPFGTRCMEGNPIPDTPCQ 60
 FGKYPSELQPWMYNE YTFVSNDAPEDTGTELLNALTDPFGTRCMEGNPIPDTPCQ
 Sbjct: 428 FGKYPSELQPWMYNEQYTFVSNDAPEDTGTELLNALTDPFGTRCMEGNPIPDTPCQ 487

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWMTQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWMTQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 488 AGEEEWTTAPVPQTIMDLFQNGNWMTQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 547

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 180
 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE
 Sbjct: 548 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 607

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDT+NNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 608 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTKNNVKVWFNNKGWHAISSFLNVIN 667

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 668 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 711

[>] >gi|4128033|emb|CAA10005.1| [>] ATP-binding cassette transporter-1 (ABC-1) [Homo s
 gi|5734101|gb|AAD49849.1|AF165281_1| [>] ATP cassette binding transporter 1 [Homo sa
 Length = 2201

Score = 585 bits (1507), Expect = e-166
 Identities = 281/284 (98%), Positives = 281/284 (98%)

Query: 1 FGKYPSELQPWMYNEFYTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELQPWMYNE YTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQ
 Sbjct: 1311 FGKYPSELQPWMYNEQYTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQ 1370

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1371 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPPQRK 1430

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIIVVNEFRYGGFSLGVSNQALPPSQE 180
 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIIVVNEFRYGGFSLGVSNQALPPSQE
 Sbjct: 1431 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIIVVNEFRYGGFSLGVSNQALPPSQE 1490

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 1491 VNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 1550

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTTSVD
 Sbjct: 1551 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVD 1594

[>] >gi|13123945|sp|095477|ABC1_HUMAN| ATP-binding cassette, sub-family A, member 1
 transporter 1 (ATP-binding cassette 1) (ABC-1)
 (Cholesterol efflux regulatory protein)
 Length = 2261

Score = 585 bits (1507), Expect = e-166
 Identities = 281/284 (98%), Positives = 281/284 (98%)

Query: 1 FGKYPSELQPWMYNEFYTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELQPWMYNE YTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQ
 Sbjct: 1371 FGKYPSELQPWMYNEQYTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQ 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1431 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIIVVNEFRYGGFSLGVSNQALPPSQE 180
 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIIVVNEFRYGGFSLGVSNQALPPSQE
 Sbjct: 1491 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIIVVNEFRYGGFSLGVSNQALPPSQE 1550

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 240
 VNDA KQMKKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN
 Sbjct: 1551 VNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVA MTTSVD
 Sbjct: 1611 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVD 1654

[>] >gi|7304849|ref|NP_038482.1| [■] ATP-binding cassette 1, sub-family A, member 1; 1 [Mus musculus]
gi|1082238|pir||A54774 ATP binding cassette transporter ABC1 - mouse
gi|495257|emb|CAA53530.1| [■] ABC transporter [Mus musculus]
 Length = 2201

Score = 549 bits (1414), Expect = e-155
 Identities = 263/284 (92%), Positives = 273/284 (96%)

Query: 1 FGKYPSELQPWEMYNEYTFVSNDAPEDGTLELLNALTDPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELQPWEMYNE YTFVSNDAPED GT ELLNALTDPGFGTRCMEGNPIPDTPC
 Sbjct: 1311 FGKYPSELQPWEMYNEQYTFVSNDAPEDMTQELLNALTDPGFGTRCMEGNPIPDTPC 1370

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSACQCSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1371 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSDKIKKMLPVCPPGAGGLPPPQRK 1430

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSN+QALPPS E 180
 Q TADILQ+LTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSN+QALPPS E
 Sbjct: 1431 QKTADILQNLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVNSQALPPSHE 1490

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 240
 VNDAIKQMKK LKL KD+SADRFL+SLGRFM GLDT+NNVKWFNNKGWHAISSFLNVIN
 Sbjct: 1491 VNDAIKQMKKLLKLTKDTSADRFLSSLGRFMAGLDKNNVKWFNNKGWHAISSFLNVIN 1550

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1551 NAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1594

[>] >gi|13124694|sp|P41233|ABC1_MOUSE ATP-binding cassette, sub-family A, member 1 transporter 1) (ATP-binding cassette 1) (ABC-1)
 Length = 2261

Score = 549 bits (1414), Expect = e-155
 Identities = 263/284 (92%), Positives = 273/284 (96%)

Query: 1 FGKYPSELQPWEMYNEYTFVSNDAPEDGTLELLNALTDPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELQPWEMYNE YTFVSNDAPED GT ELLNALTDPGFGTRCMEGNPIPDTPC
 Sbjct: 1371 FGKYPSELQPWEMYNEQYTFVSNDAPEDMTQELLNALTDPGFGTRCMEGNPIPDTPC 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQCSDKIKKMLPVCPPGAGGLPPPQRK 120
 AGEE+WT +PVPQ+I+DLFQNGNWTM+NPSACQCSDKIKKMLPVCPPGAGGLPPPQRK
 Sbjct: 1431 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSDKIKKMLPVCPPGAGGLPPPQRK 1490

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSN+QALPPS E 180
 Q TADILQ+LTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSN+QALPPS E
 Sbjct: 1491 QKTADILQNLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVNSQALPPSHE 1550

Query: 181 VNDAIKQMCKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDAIKQMCKK LKL KD+SADRFL+SLGRFM GLDT+NNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 1551 VNDAIKQMCKKLLKLTKDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVIN 1610

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1611 NAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1654

[>] >gi|11611825|gb|AAG39073.1|AF287263_1 [>] ATP-binding cassette 1, sub-family A, member 6
 Length = 2198

Score = 541 bits (1394), Expect = e-153
 Identities = 262/284 (92%), Positives = 271/284 (95%), Gaps = 2/284 (0%)

Query: 1 FGKYPSELQPWMYNE NYTFVSNDAPEDTGTLELLNALT KDPGFTRCMEGNPIPDTPCQ 60
 FGKYPSELQPWMYNE YTFVSNDAPED GT ELLNALT KDPGFTRCMEGNPIPDTPC
 Sbjct: 1311 FGKYPSELQPWMYNE QYTFVSNDAPEDMGTQELLNALT KDPGFTRCMEGNPIPDTPC 1370

Query: 61 AGEEEWT TAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKML P V C P P G A G G L P P P Q R K 120
 AGEE+WT +PVPQ+I+DLFQNGNWTM+N PSPACQCSSDKIKKML P V C P P G A G G L P P P Q R K
 Sbjct: 1371 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKML P V C P P G A G G L P P P Q R K 1430

Query: 121 QNTADILQDLTGRNIS DYLVKTYVQII AKSLKNKI WVN EFRYGGFSLGVSN TQALPPSQE 180
 Q TADILQ+LTGRNIS DYLVKTYVQII AKSLKNKI WVN EFRYGGFSLGVSN+QALPPS E
 Sbjct: 1431 QKTADILQNL TGRNIS DYLVKTYVQII AKSLKNKI WVN EFRYGGFSLGVSN QALPPSHE 1490

Query: 181 VNDAIKQMCKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VNDAIKQMCKK LKL K SADRFL+SLGRFM GLDT+NNVKVWFNNKGWHAISSFLNVIN
 Sbjct: 1491 VNDAIKQMCKKLLKLTK--SADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVIN 1548

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NAILRANLQKGENPS YGITAFNHPLNLTKQQLSEVALMTTSVD
 Sbjct: 1549 NAILRANLQKGENPSQYGITAFNHPLNLTKQQLSEVALMTTSVD 1592

[>] >gi|27714435|ref|XP_232954.1| [>] similar to ABCA1 [Homo sapiens] [Rattus norvegicus]
 Length = 978

Score = 498 bits (1283), Expect = e-140
 Identities = 239/262 (91%), Positives = 252/262 (96%)

Query: 1 FGKYPSELQPWMYNE NYTFVSNDAPEDTGTLELLNALT KDPGFTRCMEGNPIPDTPCQ 60
 FGKYP+LELQPWMYNE YTFVSNDAPED GT ELLNALT KDPGFTRCMEGNPIP+TPC
 Sbjct: 61 FGKYPNLELQPWMYNE QYTFVSNDAPEDMGTQELLNALT KDPGFTRCMEGNPIPNTPC 120

Query: 61 AGEEEWT TAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKML P V C P P G A G G L P P P Q R K 120
 GEE+WTT PVPQT+MDLFQNGNWTM+N PSP+CQCSSDKIKKML P V C P P G A G G L P P P Q R K
 Sbjct: 121 VGEEDWTG P VPQTLM DLFQNGNWTMKNPSPSCQCSSDKIKKML P V C P P G A G G L P P P Q R K 180

Query: 121 QNTADILQDLTGRNIS DYLVKTYVQII AKSLKNKI WVN EFRYGGFSLGVSN TQALPPSQE 180
 Q TADILQ+LTGRNIS DYLVKTYVQII AKSLKNK+ WVN EFRYGGFSLGVSN++QALPPSQE
 Sbjct: 181 QKTADILQNL TGRNIS DYLVKTYVQII AKSLKNK WVN EFRYGGFSLGVSDSQALPPSQE 240

Query: 181 VNDAIKQMCKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
 VN+AIKQMCKK LKL KDSSADRFL+SLGRFMTGLDT+NNVKVWFNNKGWHAISSFLNVIN

Sbjct: 241 VNNAIKQMKKLLKLTKDSSADRFLSSLGRFMTGLDTKNNVKVWFNNKGWHAISSFLNVIN 300

Query: 241 NAILRANLQKGENPSHYGITAF 262

NAILRANLQKGENPS YGITAF

Sbjct: 301 NAILRANLQKGENPSQYGITAF 322

[>gi|18028983|gb|AAL56247.1|AF362377_1] ATP-binding cassette transporter 1 [Gallus]
Length = 2260

Score = 472 bits (1215), Expect = e-132

Identities = 223/284 (78%), Positives = 256/284 (90%), Gaps = 1/284 (0%)

Query: 1 FGKYPSELQPWEMYNEYTFVSNDAPEDGTLELLNALTDPGFTRCMEGNPIPDTPCQ 60
FGKYPSELQPWEMY+E YTF+SNDAPED GT +LL+AL PGFGTRCM+G+ IPDTPC

Sbjct: 1371 FGKYPSELQPWEMYDEQYTFISNDAPEDAGTQKLLDALLNKPGFGTRCMQGHSSIPDTPC 1430

Query: 61 AGEEEWTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPPQRK 120
G++EWTTA VP +++++ + GNW+M+NPS+C+CS+ + KIKKMLPVCPPGAGGLPPPQR+

Sbjct: 1431 VGQKEWTTASVPDSVLEILR-GNWSMENPSPSCECSNEKIKKMLPVCPPGAGGLPPPQR 1489

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVNTQALPPSQE 180
Q+TADILQ+LTGRNISDYLVKTIV QII KSLKNKIWVNEFRYGGFSLG ++ LPPS E

Sbjct: 1490 QDTADILQNLTGRNISDYLVKTIVQIIIGKSLKNKIWVNEFRYGGFSLGARSSHVLPPSNE 1549

Query: 181 VNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVIN 240
V DAIKQ+KK L+LA+ SS DRFLN+L FM GLDT+NNVKVWFNNKGWHAIS+SFLNVIN

Sbjct: 1550 VTDAIKQVKKILELAQGSSGDRFLNNLASFMKGLDTKNNVKVWFNNKGWHAISFLNVIN 1609

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284

NAILRANLQ+G+NPS YGITAFNHPLNLTKQQLSEVALMTTSVD

Sbjct: 1610 NAILRANLQQGKNPSAYGITAFNHPLNLTKQQLSEVALMTTSVD 1653

[>gi|27806343|ref|NP_776646.1|] ATP-binding cassette, sub-family A (ABC1), member
gi|1943947|gb|AAC48716.1| ABC transporter [Bos taurus]
Length = 2281

Score = 288 bits (738), Expect = 4e-77

Identities = 137/286 (47%), Positives = 180/286 (62%), Gaps = 5/286 (1%)

Query: 1 FGKYPSELQPWEMYNEYTFVSNDAPEDGTLELLNALTDPGFTRCMEGNPIPDTPCQ 60
FG+YP+L L PWMY + YTF S D P+ L + L PGFG RC++ +P+ PC

Sbjct: 1395 FGEYPALTLHPWEMYQQYTFFSMDQPDSEWL SALADVLVNKGFGNRCLKEEWLPEFPC- 1453

Query: 61 AGEEEWTAPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPPGAGGLPPPQRK 120
W T V + L Q WT PSP+C+CS+ + MLP CP GAGGLPPPQR

Sbjct: 1454 GNSSPWKTPSVSPDVTHLLQQQKWTADQPSPSCRCSTREKLTMLPECPEGAGGLPPPQR 1513

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVNTQALPP--S 178
Q + +ILQDLT RN+SD+LVKTY +I SLK+K WVNE RYGG S+G PP

Sbjct: 1514 QRSTEILQDLTDRNVSDLVKTYPALIRSSLKSKFWVNEQRYGGISVG--GKLPAPPFTG 1571

Query: 179 QEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNV 238
+ + + + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV

Sbjct: 1572 EALVGFLSDLGQLMNVSGGPMTREAAKEMPAFLKQLETEDNIKVWFNNKGWHALVSFLNV 1631

Query: 239 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NAILRA+L K +NP YGIT + PLNLTK+QLSE+ ++TTSVD
 Sbjct: 1632 AHNAILRASLHKDKNPEEYGITVISQPLNLTKEQLSEITVLTTSD 1677

[>gi|2959643|gb|AAC05632.1] [■] rim ABC transporter [Homo sapiens]
 Length = 2273

Score = 287 bits (735), Expect = 9e-77
 Identities = 140/285 (49%), Positives = 181/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELQPWMYNENYTFVSNDAPEDGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
 FG+YP+L L PW+Y + YTF S D P L + L PGFG RC++ +P+ PC
 Sbjct: 1397 FGEYPALTLHPWIYQQYTFFSMDEPGSEQFTVLADVLLNKPGFGNRCLKEGWLPEYPC- 1455

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPGAGGLPPPQRK 120
 W T V I LFQ WT NPSP+C+CS+ + MLP CP GAGGLPPPQR
 Sbjct: 1456 GNSTPWKTPCVSPNITQLFQKQKWTQVNPSPSCRCSTREKLTMLPECPEGAGGLPPPQRT 1515

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 180
 Q T +ILQDLT RNISD+LVKTY +I SLK+K WVNE RYGG S+G +P + E
 Sbjct: 1516 QRSTEILQDLTDRNISDFLVKTYPALIRSSLKSKFWVNEQRYGGISIG-GKLPVVPIGE 1574

Query: 181 -VNDAIKQMKKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
 + + + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV
 Sbjct: 1575 ALVGFLSDLGRIMNVSGGPITREASKEIPDFLKHETEDNIKVWFNNKGWHALVSFLNVA 1634

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NAILRA+L K +P YGIT + PLNLTK+QLSE+ ++TTSVD
 Sbjct: 1635 HNAILRASLPKDRSPEEYGITVISQPLNLTKEQLSEITVLTTSD 1679

[>gi|2969966|emb|CAA75729.1] [■] ABCR [Homo sapiens]
 Length = 2273

Score = 287 bits (735), Expect = 1e-76
 Identities = 139/285 (48%), Positives = 181/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELQPWMYNENYTFVSNDAPEDGTLELLNALTKDPGFGTRCMEGNPIPDTPCQ 60
 FG+YP+L L PW+Y + YTF S D P L + L PGFG RC++ +P+ PC
 Sbjct: 1397 FGEYPALTLHPWIYQQYTFFSMDEPGSEQFTVLADVLLNKPGFGNRCLKEGWLPEYPC- 1455

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPGAGGLPPPQRK 120
 W T V I LFQ WT NPSP+C+CS+ + MLP CP GAGGLPPPQR
 Sbjct: 1456 GNSTPWKTPSVSPNITQLFQKQKWTQVNPSPSCRCSTREKLTMLPECPEGAGGLPPPQRT 1515

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQE 180
 Q + +ILQDLT RNISD+LVKTY +I SLK+K WVNE RYGG S+G +P + E
 Sbjct: 1516 QRSTEILQDLTDRNISDFLVKTYPALIRSSLKSKFWVNEQRYGGISIG-GKLPVVPIGE 1574

Query: 181 -VNDAIKQMKKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
 + + + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV
 Sbjct: 1575 ALVGFLSDLGRIMNVSGGPITREASKEIPDFLKHETEDNIKVWFNNKGWHALVSFLNVA 1634

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NAILRA+L K +P YGIT + PLNLTK+QLSE+ ++TTSVD
 Sbjct: 1635 HNAILRASLPKDRSPEEYGITVISQPLNLTKEQLSEITVLTTSD 1679

[>gi|6707663|sp|P78363|ABCR_HUMAN Retinal-specific ATP-binding cassette transporter) (RIM protein) (RMP) (Stargardt disease protein)
Length = 2273

Score = 287 bits (734), Expect = 1e-76
Identities = 139/285 (48%), Positives = 181/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELQPWMYNE NYTFVSNDAPEDTGTLELLNALT KDPGFGTRCMEGNPI PDTPCQ 60
 FG+YP+L L PW+Y + YTF S D P L + L PGFG RC++ +P+ PC
Sbjct: 1397 FGEYPALTLHPWIYQQYTFFSMDEPGSEQFTVLADVLLNKPGFGNRCLKEGWLPEYPC- 1455

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 W T V I LFQ WT NPSP+C+CS+ + MLP CP GAGGLPPPQR
Sbjct: 1456 GNSTPWKTPSVSPNITQLFQKQWTQVNPSPSCRCSTREKLTMLPECPEGAGGLPPPQRT 1515

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSN TQALPPSQE 180
 Q + +ILQDLT RNISD+LVKTY +I SLK+K WVNE RYGG S+G +P + E
Sbjct: 1516 QRSTEILQDLTDRNISDFLVKTYPALIRSSLKSKFWVNEQRYGGISIG-GKLPVV PITGE 1574

Query: 181 -VNDAIKQM KKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHA ISSFLNVI 239
 + + + + + ++ + F+ L+T +N+KVWFNNKGWHA+ SFLNV
Sbjct: 1575 ALVGFLSDLGRIMNVSGGPITREASKEIPDFLKHE TEDNIKVFNFNNKGWHALVSFLNVA 1634

Query: 240 NNAILRANLQKGENP SHYGITA FNHPLNLTKQQLSEVALMTTSVD 284
 +NAILRA+L K +P YGIT + PLNLTK+QLSE+ ++TTSD
Sbjct: 1635 HNAILRASLPKDRSPEEY GITVISQPLNLTKEQLSEITVLTTSD 1679

[>gi|4557876|ref|NP_000341.1] [&] ATP-binding cassette, sub-family A member 4; ATP transporter; ATP-binding transporter, retina-specific; rim protein [Homo sapiens]
gi|1888527|gb|AAC51144.1| [&] ATP-binding cassette transporter [Homo sapiens]
Length = 2273

Score = 287 bits (734), Expect = 1e-76
Identities = 139/285 (48%), Positives = 181/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELQPWMYNE NYTFVSNDAPEDTGTLELLNALT KDPGFGTRCMEGNPI PDTPCQ 60
 FG+YP+L L PW+Y + YTF S D P L + L PGFG RC++ +P+ PC
Sbjct: 1397 FGEYPALTLHPWIYQQYTFFSMDEPGSEQFTVLADVLLNKPGFGNRCLKEGWLPEYPC- 1455

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
 W T V I LFQ WT NPSP+C+CS+ + MLP CP GAGGLPPPQR
Sbjct: 1456 GNSTPWKTPSVSPNITQLFQKQWTQVNPSPSCRCSTREKLTMLPECPEGAGGLPPPQRT 1515

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSN TQALPPSQE 180
 Q + +ILQDLT RNISD+LVKTY +I SLK+K WVNE RYGG S+G +P + E
Sbjct: 1516 QRSTEILQDLTDRNISDFLVKTYPALIRSSLKSKFWVNEQRYGGISIG-GKLPVV PITGE 1574

Query: 181 -VNDAIKQM KKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHA ISSFLNVI 239
 + + + + + ++ + F+ L+T +N+KVWFNNKGWHA+ SFLNV
Sbjct: 1575 ALVGFLSDLGRIMNVSGGPITREASKEIPDFLKHE TEDNIKVFNFNNKGWHALVSFLNVA 1634

Query: 240 NNAILRANLQKGENP SHYGITA FNHPLNLTKQQLSEVALMTTSVD 284

+NAILRA+L K +P YGIT + PLNLTK+QLSE+ ++TTSVD
 Sbjct: 1635 HNAILRASLPKDRSPEEYGITVISQPLNLTKEQLSEITVLTTSDV 1679

[>] >gi|3243082|gb|AAC23915.1| [>] ATP-binding cassette transporter [Homo sapiens]
 Length = 2273

Score = 287 bits (734), Expect = 1e-76
 Identities = 139/285 (48%), Positives = 181/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELQPWMYNENYTFVSNDAPEDGTLELLNALTKDPFGTRCMEGNPIPDTPCQ 60
 FG+YP+L L PW+Y + YTF S D P L + L PGFG RC++ +P+ PC
 Sbjct: 1397 FGEYPALTLHPWIYGQQYTFFSMDEPGSEQFTVLADVLLNKPGFGNRCLKEGWLPEYPC- 1455

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPGAGGLPPPQRK 120
 W T V I LFQ WT NPSP+C+CS+ + MLP CP GAGGLPPPQR
 Sbjct: 1456 GNSTPWKTPSVSPNITQLFQKQKWTQVNPSPSCRCSTREKLTMLPECPEGAGGLPPPQRT 1515

Query: 121 QNTADILQDLTGRNIISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVNSNTQALPPSQE 180
 Q + +ILQDLT RNISD+LVKTY +I SLK+K WVNE RYGG S+G +P + E
 Sbjct: 1516 QRSTEILQDLTDRNISDFLVKTYPALIRSSLKSKFWVNEQRYGGISIG-GKLPVVPIGE 1574

Query: 181 -VNDAIKQMKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
 + + + + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV
 Sbjct: 1575 ALVGFLSDLGRIMNVSGGPITREASKEIPDFLKHETEDNIKVWFNNKGWHALVSFLNVA 1634

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NAILRA+L K +P YGIT + PLNLTK+QLSE+ ++TTSVD
 Sbjct: 1635 HNAILRASLPKDRSPEEYGITVISQPLNLTKEQLSEITVLTTSDV 1679

[>] >gi|6671495|ref|NP_031404.1| [>] ATP-binding cassette, sub-family A, member 4; ATI
 10; Rim protein [Mus musculus]

gi|2547314|gb|AAC23916.1| [>] ATP-binding cassette transporter [Mus musculus]
 Length = 2310

Score = 286 bits (731), Expect = 3e-76
 Identities = 138/285 (48%), Positives = 182/285 (63%), Gaps = 3/285 (1%)

Query: 1 FGKYPSELQPWMYNENYTFVSNDAPEDGTLELLNALTKDPFGTRCMEGNPIPDTPCQ 60
 FG++P+L L PWMY YTF S D P + L + L PGFG RC++ +P+ PC
 Sbjct: 1396 FGEFPALTLHPWMYGHQYTFFSMDEPNNEHLEVADVLLNRPGFGNRCLKEEWLPEYPC- 1454

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPGAGGLPPPQRK 120
 W T V I LFQ WT +PSP+C+CS+ + MLP CP GAGGLPPPQR
 Sbjct: 1455 INATSWKTPSVSPNITHLFQKQKWTAAHPSPSCKCSTREKLTMLPECPEGAGGLPPPQRT 1514

Query: 121 QNTADILQDLTGRNIISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVNSNTQALPPSQE 180
 Q + ++LQDLT RNISDYLVKTY +I SLK+K WVNE RYGG S+G A+P S E
 Sbjct: 1515 QRSTEVLQDLTNRNIISDYLVKTYPALIRSSLKSKFWVNEQRYGGISIG-GKLPAIPISE 1573

Query: 181 -VNDAIKQMKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVI 239
 + + + + + + + + + F+ L+T +N+KVWFNNKGWHA+ SFLNV
 Sbjct: 1574 ALVGFLSGLGQMMNVSGGPVTREASKEMLDFLKHEETTDNIKVWFNNKGWHALVSFLNVA 1633

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NAILRA+L + +P YGIT + PLNLTK+QLS++ ++TTSVD

Sbjct: 1634 HNAILRASLPRDRDPEEYGITVISQPLNLTKQLSDITVLTTSVD 1678

[gi|12656651|gb|AAK00959.1|AF328787_1] ABC transporter member 7 [Homo sapiens]
Length = 2146

Score = 244 bits (622), Expect = 1e-63
Identities = 126/284 (44%), Positives = 176/284 (61%), Gaps = 11/284 (3%)

Query: 1 FGKYPSELQPMYNEYTFVSNDAPEDGTLELLNALTKDPFGTRCMEGNPIPDTPCQ 60
FG YP+L L P MY +F S DAP D G LL AL ++ G + + P Q
Sbjct: 1263 FGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARLLEALLQEAG-----LEPPVQ 1312

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
++ VP + + +GNWT ++PSPACQCS ++++LP CP AGG PPPQ
Sbjct: 1313 HSSHRFSAPEVPAEVAKVLASNWTPESPSPACQCSRPGARRLLPDCPAAAGGPPPPQAV 1372

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVNSNTQALPPSQE 180
+ +++Q+LTGRN+SD+LVKTY +++ + LK K WVNE RYGGFSLG LP QE
Sbjct: 1373 TGSGEVVQNLTGRNLSDFLVKTPRLVRQGLKTKWWNEVRYGGFSLG-GRDPGLPSGQE 1431

Query: 181 VNDAIKQMKKHLKLAQDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 240
+ +++++ L + DR L +L + LD +++++K+WFNNKGWH++ +F+N +
Sbjct: 1432 LGRSVEELWALLSPLPGALDRVLRQGLKTKWWNEVRYGGFSLG-GRDPGLPSGQE 1491

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
NAILRA+L G + IT NHPLNLTK+QLSE ALM +SVD
Sbjct: 1492 NAILRAHLPPGPGRAHHSITTLNHPNLNTKEQLSEAALMASSVD 1535

[gi|15451838|ref|NP_150651.1] ATP-binding cassette, sub-family A, member 7, isoform SS-N; macrophage ABC transporter [Homo sapiens]
gi|15042034|dbj|BAB62294.1] ABCA-SSN [Homo sapiens]
Length = 2008

Score = 243 bits (619), Expect = 3e-63
Identities = 125/284 (44%), Positives = 175/284 (61%), Gaps = 11/284 (3%)

Query: 1 FGKYPSELQPMYNEYTFVSNDAPEDGTLELLNALTKDPFGTRCMEGNPIPDTPCQ 60
FG YP+L L P MY +F S DAP D G LL AL ++ G + + P Q
Sbjct: 1125 FGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARLLEALLQEAG-----LEPPVQ 1174

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRK 120
++ VP + + +GNWT ++PSPACQCS ++++LP CP AGG PPPQ
Sbjct: 1175 HSSHRFSAPEVPAEVAKVLASNWTPESPSPACQCSRPGARRLLPDCPAAAGGPPPPQAV 1234

Query: 121 QNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIWVNEFRYGGFSLGVNSNTQALPPSQE 180
+ +++Q+LTGRN+SD+LVKTY +++ + LK K WVNE RYGGFSLG LP QE
Sbjct: 1235 TGSGEVVQNLTGRNLSDFLVKTPRLVRQGLKTKWWNEVRYGGFSLG-GRDPGLPSGQE 1293

Query: 181 VNDAIKQMKKHLKLAQDSSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 240
+ +++++ L + DR L +L + LD +++++K+WFNNKGWH++ +F+N +
Sbjct: 1294 LGRSVEELWALLSPLPGALDRVLRQGLKTKWWNEVRYGGFSLG-GRDPGLPSGQE 1353

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
NAILRA+L G + IT NHPLNLTK+QL E ALM +SVD
Sbjct: 1354 NAILRAHLPPGRARAHHSITTLNHPNLNTKEQLFEAALMASSVD 1397

[>gi|9506365|ref|NP_061985.1|] [■] ATP-binding cassette, sub-family A, member 7, isoform SS-N; macrophage ABC transporter [Homo sapiens]
 gi|9211112|gb|AAF85794.1|AF250238_1 [■] macrophage ABC transporter [Homo sapiens]
 Length = 2146

Score = 242 bits (617), Expect = 5e-63
 Identities = 125/284 (44%), Positives = 175/284 (61%), Gaps = 11/284 (3%)

Query: 1 FGKYPSELQPMYNNENYTFVSNDAPEDGTLELLNALT KDPGFGTRCMEGNPIPDTPCQ 60
 FG YP+L L P MY +F S DAP D G LL AL ++ G + + P Q
 Sbjct: 1263 FGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARLLEALLQEAG-----LEEPVQ 1312

Query: 61 AGEEEWTATPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPGAGGLPPPQRK 120
 ++ VP + + +GNWT ++PSPACQCS +++LP CP AGG PPPQ
 Sbjct: 1313 HSSHRFSAPEVPAEVAKVLASGNWTPESPSPACQCSQPGARRLLPDCPAAAGGPPPPQAV 1372

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSN TQALPPSQE 180
 + + + + Q+LTGRN+SD+LVKTY + + + LK K WVNE RYGGFSLG LP QE
 Sbjct: 1373 TGSGEVVQNLTGRNLSDFLVKTYPRLVRQGLKTKWVNEVRYGGFSLG-GRDPGLPSQ 1431

Query: 181 VNDAIKQMKKHLKLA KDSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 240
 + + + + + L + DR L + L + LD + + + K+W FNNKGWH++ +F+N +
 Sbjct: 1432 LGRSVEELWALLSPLPGGALDRVLK NLTAWAHSLDAQDSLKIWFNNKGWHSMVA FVN RAS 1491

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLT KQQLSEVALMTTSVD 284
 NAILRA+L G + IT NHPLNLTK+QL E ALM +SVD
 Sbjct: 1492 NAILRAHLPPGRARHAHSITTLNHPLNLTKEQLFEAALMASSVD 1535

[>gi|22725156|gb|AAN04657.1|] [■] ABC transporter ABCA7 [Homo sapiens]
 Length = 2146

Score = 241 bits (615), Expect = 8e-63
 Identities = 125/284 (44%), Positives = 175/284 (61%), Gaps = 11/284 (3%)

Query: 1 FGKYPSELQPMYNNENYTFVSNDAPEDGTLELLNALT KDPGFGTRCMEGNPIPDTPCQ 60
 FG YP+L L P MY +F S DAP D G LL AL ++ G + + P Q
 Sbjct: 1263 FGHYPALRLSPTMYGAQVSFFSEDAPGDPGRARLLEALLQEAG-----LEEPVQ 1312

Query: 61 AGEEEWTATPVPQTIMDLFQNGNWTMQNPSPACQCSDKIKKMLPVCPGAGGLPPPQRK 120
 ++ VP + + +GNWT ++PSPACQCS +++LP CP AGG PPPQ
 Sbjct: 1313 HSSHRFSAPEVPAEVAKVLASGNWTPESPSPACQCSQPGARRLLPDCPAAAGGPPPPQAV 1372

Query: 121 QNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSN TQALPPSQE 180
 + + + + Q+LTGRN+SD+LVKTY + + + LK K WVNE RYGGFSLG LP QE
 Sbjct: 1373 TGSGEVVQNLTGRNLSDFLVKTYPRLVRQGLKTKWVNEVRYGGFSLG-GRDPGLPSQ 1431

Query: 181 VNDAIKQMKKHLKLA KDSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFLNVIN 240
 + + + + + L + DR L + L + LD + + + K+W FNNKGWH++ +F+N +
 Sbjct: 1432 LGRSVEELWALLSPLPGGALDRVLK NLTAWAHSLDAQDSLKIWFNNKGWHSMVA FVN RAS 1491

Query: 241 NAILRANLQKGENPSHYGITAFNHPLNLT KQQLSEVALMTTSVD 284
 NAILRA+L G + IT NHPLNLTK+QL E ALM +SVD
 Sbjct: 1492 NAILRAHLPPGPARHAHSITTLNHPLNLTKEQLFEAALMASSVD 1535

[>gi|15451840|ref|NP_038878.1| ATP-binding cassette, sub-family A, member 7 [Mus musculus]
 gi|14209834|gb|AAK56862.1|AF287141_1 ATP-binding cassette transporter sub-family A member 1
 gi|14209836|gb|AAK56863.1| ATP-binding cassette transporter sub-family A member 2
 Length = 2159

Score = 239 bits (610), Expect = 3e-62
 Identities = 128/285 (44%), Positives = 176/285 (61%), Gaps = 2/285 (0%)

Query: 1 FGKYPSELQPWMYNE NYTFVSNDAPEDTGTLELLNALT KDPGFGTRCMEGNPIPDTPCQ 60
 FG+YP L+L P MY +F S DAP D ++LL AL + G M+ + C
 Sbjct: 1266 FGQYPPQLSPAMYGPQVSFFSEDAPGDPNRMKLLEALLGEAGLQEPMQDKDARGSECT 1325

Query: 61 AGEEEWTTAP-VPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPPQ 119
 + T P VP + + +GNWT ++PSPACQCS + +LP CP GAGG PPPQ
 Sbjct: 1326 HSLACYFTVPEVPPDVASILASGNWTPESPSPACQCSQPGARRLLPDCPAGAGGPPPPQA 1385

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSN TQALPPSQ 179
 +++Q+LTGRN+SD+LVKY ++ + LK K WV+E RYGGFSLG + LP
 Sbjct: 1386 VAGLGEVVQNLTGRNVSDLFLVKTYP SLVRRGLKTKWVDEVRYGGFSLGGRDPD-LPTGH 1444

Query: 180 EVNDAIKQM KKHLKLAKDSSADRFLNSLGRFMTGLDTRNNV KW FNNKGWHAISSFLNVI 239
 EV + + + L ++ DR LN+L ++ GLD RN++K+WFNNKGWHAI +F+N
 Sbjct: 1445 EVVRTLAEIRALLSPQPGNALDRILNNLTQWALGLDARNLSKIWFNNKGWHAMVA FNRA 1504

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NN +L A L G + IT NHPLNLTK+QLSE L+ +SVD
 Sbjct: 1505 NNGLLHALLPSGPVRHAHSITTLNHPNLNTKEQLSEATLIASSVD 1549

[>gi|26342298|dbj|BAC34811.1| unnamed protein product [Mus musculus]
 Length = 1487

Score = 228 bits (582), Expect = 7e-59
 Identities = 97/107 (90%), Positives = 102/107 (95%)

Query: 1 FGKYPSELQPWMYNE YTFVSNDAPED GT ELLNALT KDPGFGTRCMEGNPIPDTPCQ 60
 FGKYPSELQPWMYNE YTFVSNDAPED GT ELLNALT KDPGFGTRCMEGNPIPDTPC
 Sbjct: 1371 FGKYPSELQPWMYNE QYTFVSNDAPED MG TQELLNALT KDPGFGTRCMEGNPIPDTPC 1430

Query: 61 AGEEEWTTAPVPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVC 107
 AGEE+WT +PVPQ+I+DLFQNGNWTM+N PSPACQCSSDKIKKMLPVC
 Sbjct: 1431 AGEEDWTISPVPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVC 1477

[>gi|20521748|dbj|BAA83014.2| KIAA1062 protein [Homo sapiens]
 Length = 1771

Score = 99.8 bits (247), Expect = 4e-20
 Identities = 72/219 (32%), Positives = 104/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTM QNPSPACQCSSDKIKKMLPVCPPGAGGLPP 116
 P AG E WT+AP +P+ + + C CS+ CP GG P
 Sbjct: 952 PPTAGPEMWTSA PSLPRLVREPVR-----CTCSAQGTGFS---CPSSVGG-HP 995

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N
 Sbjct: 996 PQMRVVTGDLTDITGHNVSEYLLFT-----SDRFRL---HRYGAITFG--NVLKSI 1042

Query: 177 PSQEVDNAIKQMKKHLKLAQDSSADRFLNSLGRFMTGLDTRNNVWFKVWFNNKGWHAISSSL 236
 P+ A ++K + R +V++NNKG+H++ ++L
 Sbjct: 1043 PASFGTRAPPVMVRK-----IAVRRAAQVFYNNKGYHSMPTYL 1079

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
 N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 1080 NSLNNAAILRANLPKSKGNAAYGITVTNHPMNKTASLS 1118

[] >gi|11346269|pir||A59189 ATP-binding cassette transporter - human (fragment)
 Length = 1529

Score = 98.2 bits (243), Expect = 1e-19
 Identities = 72/219 (32%), Positives = 104/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPP 116
 P AG E WT+AP +P+ + + C CS+ CP GG P
 Sbjct: 710 PPTAGPEMWTSAPSLPRLVREPVR-----CTCSAQGTGFS---CPSSVGG-HP 753

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N
 Sbjct: 754 PQMRVVTGDLTDITGHNVSEYLLFT-----SDRFRL---HRYGAITFG--NVLKSI 800

Query: 177 PSQEVDNAIKQMKKHLKLAQDSSADRFLNSLGRFMTGLDTRNNVWFKVWFNNKGWHAISSSL 236
 P+ A ++K + R +V++NNKG+H++ ++L
 Sbjct: 801 PASFGTRAPPVMVRK-----IAVRRAAQVFYNNKGYHSMPTYL 837

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
 N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 838 NSLNNAAILRANLPKSKGNAAYGITVTNHPMNKTASLS 876

[] >gi|14916523|sp|Q9BZC7|ABC2_HUMAN ATP-binding cassette, sub-family A, member 2
 transporter 2) (ATP-binding cassette 2)
 gi|13173236|gb|AAK14335.1| [] ABC transporter ABCA2 [Homo sapiens]
 Length = 2436

Score = 98.2 bits (243), Expect = 1e-19
 Identities = 72/219 (32%), Positives = 104/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPP 116
 P AG E WT+AP +P+ + + C CS+ CP GG P
 Sbjct: 1617 PPTAGPEMWTSAPSLPRLVREPVR-----CTCSAQGTGFS---CPSSVGG-HP 1660

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N
 Sbjct: 1661 PQMRVVTGDLTDITGHNVSEYLLFT-----SDRFRL---HRYGAITFG--NVLKSI 1707

Query: 177 PSQEVDNAIKQMKKHLKLAQDSSADRFLNSLGRFMTGLDTRNNVWFKVWFNNKGWHAISSSL 236
 P+ A ++K + R +V++NNKG+H++ ++L
 Sbjct: 1708 PASFGTRAPPVMVRK-----IAVRRAAQVFYNNKGYHSMPTYL 1744

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274

N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 1745 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 1783

[>gi|14550412|ref|NP_001597.1| ATP-binding cassette, sub-family A, member 2; K] sapiens]
 gi|9957467|gb|AAG09372.1|AF178941_1 ATP-binding cassette sub-family A member 2
 gi|13173186|gb|AAK14334.1|AF327657_1 ABC transporter ABCA2 [Homo sapiens]
 Length = 2436

Score = 98.2 bits (243), Expect = 1e-19
 Identities = 72/219 (32%), Positives = 104/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPP 116
 P AG E WT+AP +P+ + + + C CS+ CP GG P
 Sbjct: 1617 PPTAGPEMWTSAPlPRLVREPVR-----CTCSAQGTGFS---CPSSVGG-HP 1660

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N
 Sbjct: 1661 PQMRVVTGDLTDITGHNVSEYLLFT-----SDRFRL---HRYGAITFG--NVLSI 1707

Query: 177 PSQEVDIAKQMKKHLKLAQDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 236
 P+ A ++K + R +V++NNKG+H++ ++L
 Sbjct: 1708 PASFGTRAPPVMVRK-----IAVRRAAQVFYNNKGYHSMPTYL 1744

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
 N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 1745 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 1783

[>gi|11993939|ref|NP_031405.1| ATP-binding cassette, sub-family A (ABC1), member 2 [Mus musculus]
 gi|14916951|sp|P41234|ABC2_MOUSE ATP-binding cassette, sub-family A, member 2 (ATP transporter 2) (ATP-binding cassette 2)
 gi|11990231|emb|CAA53531.2| ABC transporter [Mus musculus]
 Length = 2434

Score = 97.4 bits (241), Expect = 2e-19
 Identities = 72/219 (32%), Positives = 103/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPP 116
 P AG E WT+AP +P+ + + + C CS+ CP GG P
 Sbjct: 1617 PPTAGPETWTSAPlPRLVHEPVR-----CTCSAQGTGFS---CPSSVGG-HP 1660

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N Q
 Sbjct: 1661 PQMRVVTGDLTDITGHNVSEYLLFT-----SDRFRL---HRYGAITFG--NVQKSI 1707

Query: 177 PSQEVDIAKQMKKHLKLAQDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 236
 P+ F + + + R +V +NNKG+H++ ++L
 Sbjct: 1708 PAS-----FGARVPPMVRKIAVRRAAQVLVYNNKGYHSMPTYL 1744

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
 N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 1745 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 1783

[>] >gi|14250599|gb|AAH08755.1|AAH08755 [>] Similar to KIAA1062 protein [Homo sapiens]
Length = 867

Score = 96.7 bits (239), Expect = 3e-19
Identities = 71/219 (32%), Positives = 103/219 (47%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMQNPSACQCSSDKIKKMLPVCPPGAGGLPP 116
P AG E WT+AP +P+ + + + C CS+ CP GG P
Sbjct: 48 PPTAGPEMWTSA~~PL~~PRLVREPVR-----CTCSAQGTGFS---CPSSVGG-HP 91

Query: 117 PQRKQNTADILQDLTGRNISDYLVKT~~V~~QIIAKSLKNK~~I~~WVN~~E~~F~~R~~YGGFSLGV~~S~~N~~T~~QALP 176
PQ + DIL D+TG N+S+YL+ T S + ++ RYG + G N
Sbjct: 92 PQM~~R~~VVAGDILTDITGHNVSEYLLFT-----SDRFRL---HRYGAITFG--NVLKSI 138

Query: 177 PSQEVDNAIKQMKHLKLA~~D~~SSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFL 236
P+ A ++K + R +V++NNKG+H++ ++L
Sbjct: 139 PASFGTRAPPVRK-----IAVRRAAQVFYNNKGYHSMPTYL 175

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
N +NNAILRANL K + NP+ YGIT NHP+N T LS
Sbjct: 176 NSLNNA~~I~~ILRANLP~~K~~SKGNPAAYGITVTNHPMNKTSASLS 214

[>] >gi|1082239|pir||B54774 ATP binding cassette transporter ABC2 - mouse (fragment)
Length = 1472

Score = 95.5 bits (236), Expect = 7e-19
Identities = 71/219 (32%), Positives = 102/219 (46%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMQNPSACQCSSDKIKKMLPVCPPGAGGLPP 116
P AG E WT+AP +P+ + + + C CS+ CP GG P
Sbjct: 654 PPTAGPETWTSA~~PL~~PRLVHEPVR-----CTCSAQGTGFS---CPSSVGG-HP 697

Query: 117 PQRKQNTADILQDLTGRNISDYLVKT~~V~~QIIAKSLKNK~~I~~WVN~~E~~F~~R~~YGGFSLGV~~S~~N~~T~~QALP 176
PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N Q
Sbjct: 698 PQM~~R~~VVTGDI~~L~~T~~D~~ITGHNVSEYLLFT-----SDRFRL---HRYGAITFG--NVQKSI 744

Query: 177 PSQEVDNAIKQMKHLKLA~~D~~SSADRFLNSLGRFMTGLDTRNNVKWFNNKGWHAISSFL 236
P+ F + + + R +V +NNKG+H++ ++L
Sbjct: 745 PAS-----FGARVPPMVRKIAVRVAQVLYNNKGYHSMPTYL 781

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
N +NNAILRANL K + NP+ Y IT NHP+N T LS
Sbjct: 782 NSLNNA~~I~~ILRANLP~~K~~SKGNPAAYXITVTNHPMNKTSASLS 820

[>] >gi|13242308|ref|NP_077372.1| [>] ATP-binding cassette, sub-family A (ABC1), member norvegicus]

gi|10799949|dbj|BAB16596.1| [>] ABC2 [Rattus norvegicus]
Length = 2434

Score = 94.7 bits (234), Expect = 1e-18
Identities = 72/219 (32%), Positives = 102/219 (46%), Gaps = 54/219 (24%)

Query: 58 PCQAGEEEWTTAP-VPQTIMDLFQNGNWTMQNPSACQCSSDKIKKMLPVCPPGAGGLPP 116

P AG E WT AP +P+ + + + C CS+ CP GG P
 Sbjct: 1617 PPTAGPETWTWAPSLPRLVHEPVR-----CTCSAQGTGFS---CPSSVGG-HP 1660

Query: 117 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNNEFRYGGFSLGVSNQALP 176
 PQ + T DIL D+TG N+S+YL+ T S + ++ RYG + G N Q
 Sbjct: 1661 PQMRVVTGDLTDITGHNVSEYLLFT-----SDRFRL---HRYGAITFG--NIQKSI 1707

Query: 177 PSQEVDNAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISFL 236
 P+ ++K + R +V +NNKG+H++ ++L
 Sbjct: 1708 PAPIGTRTPLMVRK-----IAVRRVAQVLYNNKGYHSMPTYL 1744

Query: 237 NVINNAILRANLQKGE-NPSHYGITAFNHPLNLTKQQLS 274
 N +NNAILRANL K + NP+ YGIT NHP+N T LS
 Sbjct: 1745 NSLNNAILRANLPKSKGNPAAYGITVTNHPMNKTSASLS 1783

[>gi|27881503|ref|NP_775099.1|] ATP-binding cassette, sub-family A, member 12 is
 cassette A12 [Homo sapiens]
 Length = 2347

Score = 81.6 bits (200), Expect = 1e-14
 Identities = 72/286 (25%), Positives = 123/286 (43%), Gaps = 78/286 (27%)

Query: 4 YPSLELQPWMY--NENYTFVSNDAPEDTGTLELLNALTDPGFTRCMEGNPIPDTPC-- 59
 YP +++ P +Y +E F +N P T L++A+ PG C+ + D C
 Sbjct: 1526 YPEIQISPSLYGTSEQTAFYANYHPS---TEALVSAMWDPGIDNMCLNTS---DLQCLN 1579

Query: 60 QAGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPGAGGLPPPQR 119
 + E+W T+ P T + C CS+ + CP PP R
 Sbjct: 1580 KDSLEKWNTSGEPITNFGV-----CSCSEN----VQECP--KFNYSPPHR 1618

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNNEFRYGGFSLGVSNQALPPSQ 179
 + ++ ++ +LTG+ + +YL+ T + + K RYGG+S G
 Sbjct: 1619 RTYSSQVIYNLTGQRVENYLISTANEJVQK-----RYGGWSFG----- 1656

Query: 180 EVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLD-TRNNVKVWFNNKGWHAISFLNV 238
 L L KD D +TG+ R KVW++ +G+H++ ++LN
 Sbjct: 1657 -----LPLTKDLRFD-----ITGVPAANRTLAKVWYDPEGYHSLPAYLNS 1695

Query: 239 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NN +LR N+ K + H GI ++HP + Q E A +++ +D
 Sbjct: 1696 LNNFLLRVNMSKYDAARH-GIIMYSHPYPGVQDQ--EQATISSLID 1738

[>gi|27881501|ref|NP_056472.2|] ATP-binding cassette, sub-family A, member 12 is
 cassette A12 [Homo sapiens]
 Length = 2277

Score = 81.6 bits (200), Expect = 1e-14
 Identities = 72/286 (25%), Positives = 123/286 (43%), Gaps = 78/286 (27%)

Query: 4 YPSLELQPWMY--NENYTFVSNDAPEDTGTLELLNALTDPGFTRCMEGNPIPDTPC-- 59
 YP +++ P +Y +E F +N P T L++A+ PG C+ + D C
 Sbjct: 1456 YPEIQISPSLYGTSEQTAFYANYHPS---TEALVSAMWDPGIDNMCLNTS---DLQCLN 1509

Query: 60 QAGEEEWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPGAGGLPPPQR 119
 + E+W T+ P T + C CS+ + CP PP R

Sbjct: 1510 KDSLEKWNTSGEPITNFGV-----CSCSEN----VQECP--KFNYSPPHR 1548

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQ 179
+ ++ +LTG+ + +YL+ T + + K RYGG+S G

Sbjct: 1549 RTYSSQVIYNLTGQRVENYLISTANEJVQK-----RYGGWSFG----- 1586

Query: 180 EVNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLD-TRNNVKVWFNNKGWHAISSFLNV 238
L L KD D +TG+ R KVW++ +G+H++ ++LN

Sbjct: 1587 -----LPLTKDLRFD-----ITGPANRTLAKVWYDPEGYHSLPAYLNS 1625

Query: 239 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
+NN +LR N+ K + H GI ++HP + Q E A +++ +D

Sbjct: 1626 LNNFLLRVNMSKYDAARH-GIIMYSHPYPGVQDQ--EQATISSLID 1668

[>gi|23957299|gb|AAN40735.1|AF418105_1] [■] ATP-binding cassette transporter family
Length = 2347

Score = 81.6 bits (200), Expect = 1e-14
Identities = 72/286 (25%), Positives = 123/286 (43%), Gaps = 78/286 (27%)

Query: 4 YPSLELQPWMY--NENYTFVSNDAPEDTGTLLELLNALTQDPFGTRCMEGNPIPDTPC-- 59
YP +++ P +Y +E F +N P T L++A+ PG C+ + D C

Sbjct: 1526 YPEIQISPSLYGTSEQTAFYANYHPS---TEALVSAMWDFPGIDNMCLNTS---DLQCLN 1579

Query: 60 QAGEEEWTAPVPQTIMDLFQNGNWMTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQR 119
+ E+W T+ P T + C CS + CP PP R

Sbjct: 1580 KDSLEKWNTSGEPITNFGV-----CSCSEN----VQECP--KFNYSPPHR 1618

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQ 179
+ ++ +LTG+ + +YL+ T + + K RYGG+S G

Sbjct: 1619 RTYSSQVIYNLTGQRVENYLISTANEJVQK-----RYGGWSFG----- 1656

Query: 180 EVNDAIKQMCKHLKLAKDSSADRFLNSLGRFMTGLD-TRNNVKVWFNNKGWHAISSFLNV 238
L L KD D +TG+ R KVW++ +G+H++ ++LN

Sbjct: 1657 -----LPLTKDLRFD-----ITGPANRTLAKVWYDPEGYHSLPAYLNS 1695

Query: 239 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
+NN +LR N+ K + H GI ++HP + Q E A +++ +D

Sbjct: 1696 LNNFLLRVNMSKYDAARH-GIIMYSHPYPGVQDQ--EQATISSLID 1738

[>gi|14189735|gb|AAK54355.1|] [■] ATP-binding cassette transporter family A member 1
Length = 2277

Score = 81.6 bits (200), Expect = 1e-14
Identities = 72/286 (25%), Positives = 123/286 (43%), Gaps = 78/286 (27%)

Query: 4 YPSLELQPWMY--NENYTFVSNDAPEDTGTLLELLNALTQDPFGTRCMEGNPIPDTPC-- 59
YP +++ P +Y +E F +N P T L++A+ PG C+ + D C

Sbjct: 1456 YPEIQISPSLYGTSEQTAFYANYHPS---TEALVSAMWDFPGIDNMCLNTS---DLQCLN 1509

Query: 60 QAGEEEWTAPVPQTIMDLFQNGNWMTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQR 119
+ E+W T+ P T + C CS + CP PP R

Sbjct: 1510 KDSLEKWNTSGEPITNFGV-----CSCSEN----VQECP--KFNYSPPHR 1548

Query: 120 KQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNQALPPSQ 179

+ ++ ++ +LTG+ + +YL+ T + + K RYGG+S G
 Sbjct: 1549 RTYSSQVIYNLTGQRVENYLISTANEJVQK-----RYGGWSFG----- 1586

Query: 180 EVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLD-TRNNVKVWFNNKGWHAISSFLNV 238
 L L KD D +TG+ R KVW++ +G+H++ ++LN
 Sbjct: 1587 -----LPLTKDLRFD-----ITGPANRTLAKVWYDPEGYHSLPAYLNS 1625

Query: 239 INNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 +NN +LR N+ K + H GI ++HP + Q E A +++ +D
 Sbjct: 1626 LNNFLLRVNMSKYDAARH-GIIMYSHPYPGVQDQ--EQATISSLID 1668

[gi|27684549|ref|XP_237242.1] similar to ATP-binding cassette transporter family
 sapiens] [Rattus norvegicus]
 Length = 1699

Score = 74.7 bits (182), Expect = 1e-12
 Identities = 70/285 (24%), Positives = 122/285 (42%), Gaps = 76/285 (26%)

Query: 4 YPSLELQPWMY--NENYTFVSNDAPEDTGTLELLNALT KDPGFTRCMEGNPIPDTPCQA 61
 YP L + P +Y +E F +N P T L++AL PG C+ + D+ C
 Sbjct: 878 YPELLISPSIYGNSEQTAFYANFDPS---TNALVSALWNFPGIDNVCLNTS---DSQCLK 931

Query: 62 GEE--EWTTAPVPQTIMDLFQNGNWTMQNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQR 119
 + +W T+ +D F C C SD ++ CP PP R
 Sbjct: 932 KDNLGKWNTS---GEAIDNFG-----VCSC-SDNVQE---CP--KFNYSPPHR 970

Query: 120 KQNTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIKWVNEFRYGGFSLGVSN TQALPPSQ 179
 + ++ ++ +LTG+++ +YL+ T + K RYGG+S G
 Sbjct: 971 RTYSSQVIYNLTGKHMENYLISTANHFVQK-----RYGGWSFG----- 1008

Query: 180 EVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNV 239
 +KL D D + R + KVW++ +G+H++ ++LN +
 Sbjct: 1009 -----MKLTNDLRFDTAVPVNRTLA-----KVWYDPEGYHSLPAYLNSL 1048

Query: 240 NNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
 NN +LR N+ + + H GI ++HP + Q E A +++ +D
 Sbjct: 1049 NNFLLRVNMSYEYDAARH-GIIMYSHPYPGVQDQ--EQATISSLID 1090

[gi|25141343|ref|NP_490949.2] ABC transporter family member [Caenorhabditis elegans]
 [gi|20198808|gb|AAK21369.2] Hypothetical protein F12B6.1 [Caenorhabditis elegans]
 Length = 1547

Score = 71.6 bits (174), Expect = 1e-11
 Identities = 59/188 (31%), Positives = 86/188 (45%), Gaps = 40/188 (21%)

Query: 122 NTADILQDLTGRNISDYLVKTIVQIIAKSLKNKIKWVNEFRYGGFSLGVSN TQALPPSQEV 181
 NT D + DLTGRN++ + + T +A + F GGFSLG N +A SQ
 Sbjct: 743 NTTDRIFDLTGRNLTQFRLITRFAQLANT-----TAPFFLGGFSLGHVNQRA--QSQAD 794

Query: 182 ND-----AIKQMKKHLKL-----AKDSSADRFLNSLGRFMTGL 214
 D IK + + +++ A++ + ++ +N L + L
 Sbjct: 795 IDTSKRGWLETIKDIAQSMRIINLNTT GIEPATPKVLD PFAQNI TLNQVVNDL--LQNL 851

Query: 215 DTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQKGENPSHYGITAFNHPLNL-TQQL 273
 D R NVKVFNNK W N+++NA+LR +P GI NHP+N T Q L

Sbjct: 852 DVRENVKWWFNNKIWPGFPIASNILSNALLRQE-DYAIDPEDLGILTMMNHPMNKTISQTL 910

Query: 274 SEVALMTT 281

+ AL T

Sbjct: 911 DQNALKFT 918

[]>gi|7498949|pir||T15200 hypothetical protein F12B6.1 - Caenorhabditis elegans
Length = 1447

Score = 70.9 bits (172), Expect = 2e-11

Identities = 59/188 (31%), Positives = 86/188 (45%), Gaps = 40/188 (21%)

Query: 122 NTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNNTQALPPSQEV 181

NT D + DLTGRN++ + + T +A + F GGFSLG N +A SQ

Sbjct: 743 NTTDRIFDLTGRNLTQFRLITRFAQLANT-----TAPFFLGGFSLGHVNQRA--QSQAD 794

Query: 182 ND-----AIKQMKKHLKL-----AKDSSADRFLNSLGRFMTGL 214
D IK + + +++ A++ + ++ +N L + L

Sbjct: 795 IDTSKRGWLETIKDIAQSMRIINLNNTTGIEPATPKVLDPFAQNITLNQVVNDL---LQNL 851

Query: 215 DTRNNVKWWFNNKGWHAISSFLNVINNAILRANLQKGENPSHYGITAFNHPLNLTKQQL 273

D R NVKWWFNNK W N+++NA+LR +P GI NHP+N T Q L

Sbjct: 852 DVRENVKWWFNNKIWPGFPIASNILSNALLRQE-DYAIDPEDLGILTMMNHPMNKTISQTL 910

Query: 274 SEVALMTT 281

+ AL T

Sbjct: 911 DQNALKFT 918

[]>gi|21297828|gb|EAA09973.1| agCP11808 [Anopheles gambiae str. PEST]
Length = 1725

Score = 58.5 bits (140), Expect = 1e-07

Identities = 25/63 (39%), Positives = 41/63 (65%), Gaps = 4/63 (6%)

Query: 222 VWFNNKGWHAISSFLNVINNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTT 281

VW+NNKG+H++ ++LN+++ A+LRA L N S Y I NHPL + + +LS +++

Sbjct: 1051 VWYNNKGYHSMPTWLNMLDATVLRAEL---NDSSYTIRTINHPLKIEEDELSVSSMLQQ 1106

Query: 282 SVD 284

D

Sbjct: 1107 IAD 1109

[]>gi|20850354|ref|XP_136692.1| [] similar to ATP-binding cassette transporter family
sapiens] [Mus musculus]
Length = 1670

Score = 58.2 bits (139), Expect = 1e-07

Identities = 42/165 (25%), Positives = 74/165 (44%), Gaps = 51/165 (30%)

Query: 93 CQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLK 152

C C SD +++ CP PP R+ ++ ++ +LTG+++ +YL+ T + K

Sbjct: 1533 CSC-SDNVQE---CP---KFNYHPPHRRTYSSQVIYNLTGKHMEYLITTANHFVQK--- 1582

Query: 153 NKIWWNEFRYGGFSLGVSNTQALPPSQEVNDAIKQMKKHLKLA
DRFLNSLGRFMT 212
RYGG+S G +KL D D +T
Sbjct: 1583 -----RYGGWSFG-----MKLTNDLRFD-----VT 1602

Query: 213 GL-DTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQKGENPSH 256
+ D R KVW++ +G+H++ ++LN +NN +LR N+ + + H
Sbjct: 1603 AVPDNRTLAKVWYDPEGYHSLPAYLNSLNNFLLRVNMSEYDAARH 1647

[>] >gi|24643648|ref|NP_608437.1| [>] CG1819-PA [Drosophila melanogaster]
gi|22832643|gb|AAF50847.2| [>] CG1819-PA [Drosophila melanogaster]
Length = 1591

Score = 47.0 bits (110), Expect = 3e-04
Identities = 29/92 (31%), Positives = 47/92 (51%), Gaps = 11/92 (11%)

Query: 199 SADRFLNSLGRFMT-----GLDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQKGE 252
S D LNS G + GL+ + VW+NNKG+H++ ++LN +N+ +LR +
Sbjct: 892 SYDWVLNSWGEYSERRYGGYGLNG-SGATVVYNNKGYHSMMAWLNDLNSELLRTTM---- 946

Query: 253 NPSHYGITAFNHPLNLTKQQLSEVALMTTSVD 284
N S I N P L +LS +++ + D
Sbjct: 947 NDSESSILTLNEPWKLGFAELSTSSILRQAGD 978

[>] >gi|27697650|ref|XP_223630.1| [>] similar to hypothetical protein FLJ33951 [Homo s
norvegicus]
Length = 1132

Score = 38.5 bits (88), Expect = 0.11
Identities = 15/27 (55%), Positives = 21/27 (77%)

Query: 222 VWFNNKGWHAISSFLNVINNAILRANL 248
VW+N KG+H++ S+LN +NN IL NL
Sbjct: 178 VWYNQKGFHSLPSYLNHLLNLILWQNL 204

[>] >gi|15610478|ref|NP_217859.1| hypothetical protein Rv3342 [Mycobacterium tuberc
gi|6137297|sp|O53392|YX42_MYCTU Putative methyltransferase RV3342
gi|7477581|pir||E70846 hypothetical protein Rv3342 - Mycobacterium tuberculosis
H37RV)
gi|2894252|emb|CAA17114.1| hypothetical protein Rv3342 [Mycobacterium tuberculosis
Length = 243

Score = 34.3 bits (77), Expect = 2.3
Identities = 22/88 (25%), Positives = 39/88 (44%)

Query: 21 VSNDAPEDTGTLELLNALTKDPFGTRCMEGNPIPDTPCQAGEEEWTTAPVPQTIMDLFQ 80
V N E G + L + G R P P T Q + EWT PQ ++DL
Sbjct: 134 VWNTRDERLGWVRELGEIIGRDGDPVRDRVTLPEPFTTVQRHQVEWTNYLTPQALIDLVA 193

Query: 81 NGNWTMQNPSPACQCSSDKIKKMLPVCP 108
+ ++ + +P+ + D+++++L P
Sbjct: 194 SRSYCITSPAQVRTKTLDRVRQLLATHP 221

[>gi|15842938|ref|NP_337975.1| methyltransferase, putative [Mycobacterium tuberculosis]
 gi|13883273|gb|AAK47789.1| methyltransferase, putative [Mycobacterium tuberculosis]
 Length = 236

Score = 33.9 bits (76), Expect = 2.4
 Identities = 22/88 (25%), Positives = 39/88 (44%)

Query: 21 VSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQAGEEEWTTAPVPQTIMDLFQ 80
 V N E G + L + G R P P T Q + EWT PQ ++DL
 Sbjct: 127 VWNTRDERLGVWRELGEIIGRDGDPVRDRVTLPEPFTTVQRHQVEWTNYLTPQALIDLVA 186

Query: 81 NGNWQMNPSPACQCSSDKIKKMLPVCP 108
 + ++ + +P+ + D+++++L P
 Sbjct: 187 SRSYCITSAPAQVRTKTLDRVRQLLATHP 214

[>gi|20088939|ref|NP_615014.1| conserved hypothetical protein [Methanosaerina acetivorans C2A]
 gi|19913785|gb|AAM03494.1| conserved hypothetical protein [Methanosaerina acetivo-
 rans C2A]
 Length = 345

Score = 33.9 bits (76), Expect = 2.6
 Identities = 31/114 (27%), Positives = 54/114 (47%), Gaps = 13/114 (11%)

Query: 100 IKKMLPVCPGAGGLPPPQRKQNTADILQDLTGRN-ISDYLV-----KTYVQIIAKS 150
 +K L VC P + L R + DI++D R I LV K Y ++I ++
 Sbjct: 214 LKTYLRCQPKSPAL--WDRINESLDIMDKCSRTVIRTLVKGENIFNPKGYAELIKRA 271

Query: 151 LKNKIWVNEFRYGGFSLGVSNQALPPSQEVNDAIKQMKKHL--KLAKDSSADR 202
 + + + + + GFS + A+P +EV + K++ KHL ++A +S R
 Sbjct: 272 SPDFVEIKAYMHLGFSRLDRSAMPTHEEVLEFSKELAKHLYEIADESEISR 325

[>gi|1172578|sp|Q08304|PPOB_LYCES Polyphenol oxidase B, chloroplast precursor (PI oxidase)
 gi|1076593|pir|S33540 catechol oxidase (EC 1.10.3.1) B precursor [similarity] -
 gi|22727|emb|CAA78296.1| polyphenol oxidase precursor [Lycopersicon esculentum]
 Length = 596

Score = 33.9 bits (76), Expect = 2.8
 Identities = 30/93 (32%), Positives = 44/93 (47%), Gaps = 6/93 (6%)

Query: 166 SLGVSNTQALPPSQEVNDAIKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKWVN 225
 S+G NT LPP+ EV + +M K + A + A + T NN++ ++
 Sbjct: 445 SVGKVNTSTLPPANEVF-PLAKMDKTISFAINRPASSRTQQEKNEQEEMLTFFNNIR--YD 501

Query: 226 NKGWHAISSFLVINNAILRAN-LQKGENPSHY 257
 N+G+ FLSV NN + AN L K E Y
 Sbjct: 502 NRGYIRFDVFLNVDNN--VNANELDKAEFAGSY 532

[>gi|20899064|ref|XP_139895.1| similar to ATP-binding cassette, sub-family A member 3; ABC transporter 3 [Homo sapiens] [Mus musculus]

Length = 1686

Score = 33.5 bits (75), Expect = 3.2
 Identities = 21/65 (32%), Positives = 34/65 (52%), Gaps = 5/65 (7%)

Query: 214 LDTRNNVKVWFNNKGWHAISSFLNVINNAILRANLQKGENPSHYGITAFNHPLNLTKQQL 273
 ++ VK FNN+ +H+ S L +++N + + L G N S IT N+P T ++
 Sbjct: 967 VNNHTTVKALFNNQAYHSPSLALTLVDNLLFK--LLSGANAS---ITTTNYPQPQTAIEV 1021

Query: 274 SEVAL 278
 SE L
 Sbjct: 1022 SESIL 1026

[>gi|21227448|ref|NP_633370.1| Fe-S oxidoreductase [Methanosa

rcina mazei Goe1]
 gi|20905817|gb|AAM31042.1| Fe-S oxidoreductase [Methanosa

rcina mazei Goe1]
 Length = 365

Score = 33.1 bits (74), Expect = 4.3
 Identities = 30/114 (26%), Positives = 54/114 (47%), Gaps = 13/114 (11%)

Query: 100 IKKMLPVCPGAGGLPPPQRKQNTADILQDLTGRN-ISDYLVK-----TYVQIIAKS 150
 ++ L +C P + L R + DI++D + R I LVK Y ++I K+
 Sbjct: 238 LETYLRICQPKSPAL--WDRINESLDIMDKSSRTVIRTLVKGENIFNPEGYAEMIKKA 295

Query: 151 LKNKIWVNEFRYGGFSLGVSN

TQALPPSQEVNDAIKQMKKHL--KLAKDSSADR 202
 + + + + GFS A+P +EV + K++ KHL ++A +S R
 Sbjct: 296 SPDFVEIKAYMHLGFSRLRLERSAMPSHEEVLEFSKELAKHLYEIADESEISR 349

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF

Posted date: Feb 3, 2003 1:28 AM

Number of letters in database: 424,737,763

Number of sequences in database: 1,326,269

Lambda K H
 0.315 0.133 0.407

Gapped

Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 263,239,907

Number of Sequences: 1326269

Number of extensions: 12084886

Number of successful extensions: 31048

Number of sequences better than 10.0: 58

Number of HSP's better than 10.0 without gapping: 46

Number of HSP's successfully gapped in prelim test: 12
Number of HSP's that attempted gapping in prelim test: 30923
Number of HSP's gapped (non-prelim): 75
length of query: 284
length of database: 424,737,763
effective HSP length: 122
effective length of query: 162
effective length of database: 262,932,945
effective search space: 42595137090
effective search space used: 42595137090
T: 11
A: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.6 bits)
S2: 72 (32.3 bits)